

# SEQUENCE LISTING

(1) GENERAL INFORMATION:  
(iii) NUMBER OF SEQUENCES: 5

(2) INFORMATION FOR SEQ ID No: 1  
(i) CHARACTERISTICS OF THE SEQUENCE:

(A) LENGTH:  
(B) TYPE: nucleotide  
(C) NUMBER OF STRANDS: double  
(D) CONFIGURATION: linear  
(ii) TYPE OF MOLECULE: DNA  
(ix) CHARACTERISTICS

(A) NAME/KEY:  
(xi) DESCRIPTION OF THE SEQUENCES: SEQ ID No: 1:

GAATTCAGAT GCCTCATACC TTGGGATTAA AAAATTGATG TTCATTGTGTT ATATATCCTG	60
GGCGGACAGG CCGGCTCGTA TTCTTCAGGG GTGTCGCCTA CCCAGTGCAC AGGAGGTCC	120
GGAGGTGTCT TGGATGGAAA GTAAGGCCAT TTGTGGGTTC TCATCCATGT CATCGTCCCT	180
TTCGGCTGTT TCACCAAGAT CCAATTATTC CTCCAGGACT TTCAACCCTC AGAATGGAAA	240
CAGAGATGAA ACTCTCTGTG CAAATCGTAG ATATCGATTG GAGACATTGA AACCACGGAG	300
TTTGAAATAA AAGTATAAAT ACCTCCGAAA ACGCAGAGTT TAAG ATG AAA GGT ATT	356
Met Lys Gly Ile	
1	
TCT AAG ATC CTC TCT GCC TCT ATT GCC CTG ATG AAG TTG GAG AAT GTC	404
Ser Lys Ile Leu Ser Ala Ser Ile Ala Leu Met Lys Leu Glu Asn Val	
5 10 15 20	
TAT TCA GCA ACC GCA CTG TGC AGC AAT GCA TAT GGC CTA ACT CCG GGA	452
Tyr Ser Ala Thr Ala Leu Cys Ser Asn Ala Tyr Gly Leu Thr Pro Gly	
25 30 35	
CAA CAG GGT ATG GCT CAG CAG CCG TCG TAT GTG CTG ATC CCC AGC ACC	500
Gln Gln Gly Met Ala Gln Gln Pro Ser Tyr Val Leu Ile Pro Ser Thr	
40 45 50	
CCG GGA ACC ATA GCA AAC TGT GCA AGC GGT TCA CAG GAC ACA TAT TCT	548
Pro Gly Thr Ile Ala Asn Cys Ala Ser Gly Ser Gln Asp Thr Tyr Ser	
55 60 65	
CCT TCT CCC GCT GCA CCC ACA TCT CCA GTG ACT CCG GGG AAA ACT AGC	596
Pro Ser Pro Ala Ala Pro Thr Ser Pro Val Thr Pro Gly Lys Thr Ser	
70 75 80	
GAG AAT GAG ACA TCT CCA TCG GCT CCT GCA GAA GAT GTA GGA ACA TGC	644
Glu Asn Glu Thr Ser Pro Ser Ala Pro Ala Glu Asp Val Gly Thr Cys	
85 90 95 100	
AAG ATT GCC GTA TTG AAG CAC TGC GAC GCA CCA GGA ACA ACA TCA GGG	692
Lys Ile Ala Val Leu Lys His Cys Asp Ala Pro Gly Thr Thr Ser Gly	
105 110 115	

0054520000



ATG GAG GCC TGT GCA ACA CCA ACA CCA ACG GTT ATT ATA GGC AAC AGC	1460
Met Glu Ala Cys Ala Thr Pro Thr Pro Thr Val Ile Ile Gly Asn Ser	
360 365 370	
GAG TAT CTT GTT GGA CCA GGA ATG TAC AAT GCA ATT AAC TCT CCA TGC	1508
Glu Tyr Leu Val Gly Pro Gly Met Tyr Asn Ala Ile Asn Ser Pro Cys	
375 380 385	
AAC ACT GCT GTC CAA TGC TGC TAG GCTAAAATAA AACGAGTTTA ATCTTCTTTT	1562
Asn Thr Ala Val Gln Cys Cys	
390 395	
TCTTCGGTCT TTTGGAACGT TGGATGGGGA TGGAGGAGTC TATGGGCTGA AGTGAAATGC	1622
CAACACTTCT TCTGCCCAAG AACACATTCTG GATGTTCTTC CTGTGGCCAG GAGTTTGGTA	1682
ACAGGATTCC CCGAGGATTT AGCAGCCTTG GAGTACCATG ATTGAATCAG TATTAACTT	1742
CTCAAATTAT TTTATTCTTT CTGTTTATA TCCCAGGCCA ATCTGAGAAG AATGCCTCGA	1802
ATTCAAGCTC CCTTAGAAGT GTGGGATC	1830

## (2) INFORMATION FOR SEQ ID No: 2

### (i) CHARACTERISTICS OF THE SEQUENCE:

(A) LENGTH:

(B) TYPE: nucleotide

(C) NUMBER OF STRANDS: double

(D) CONFIGURATION: linear

(ii) TYPE OF MOLECULE: DNA

(ix) CHARACTERISTICS

(A) NAME/KEY:

(xi) DESCRIPTION OF THE SEQUENCES: SEQ ID No: 2:

AAGCTTCTGA ACAAGCGCTA ACCCTCTTTC AGAATATATA AAGCAATCCA TACAACTTCT	60
CCATCCATCC CGGTGCTGTT TCTTTGGAGG CAAAACAGAG GAGGTGGCGA TATCGATGGT	120
GCATCCATAA TATATACAAG ACACTCCAGG CTGCAACTGA ATCAACACAC TCCATCCCCT	180
CAGGAAGTCG GTAAACTTGC CTTGAAAATA GCCAATGGAT GTCTCCAGGC TTTATACCAT	240
GCACAGCTAT ATCTTGGCCT GAAGTGCAC TTCAGGTGGG GCTTTGTTAC ATTGCGGTGT	300
TTTGGATTAC CTGATATAAT TTGTTACCCA CTGAGTCAAG TCGAAACCAG TAGTCCGCAG	360
ATTTCTAACA GAGAGGAAAG ACTGGAGGTA ATTTGTGGCT TTTGAAACAT GCACAGCAAA	420
ATAAAATATA AAAGAAGCCT TTTGCACACT ACCAAAG ATG TTG TTA CTT CTC GCC	475
Met Leu Leu Leu Leu Ala	
1 5	
ATA ACT GCT GTT GTT AGC GCC ACG ATG GTC CAT CCT TCA GCT GTT GTT	523
Ile Thr Ala Val Val Ser Ala Thr Met Val His Pro Ser Ala Val Val	
10 15 20	
CCA CAG CCC GCA GCA CCT CTC CAT GTC GTT CCC CCA CAG CAG CAA ATG	571
Pro Gln Pro Ala Ala Pro Leu His Val Val Pro Pro Gln Gln Gln Met	
25 30 35	
GGC ATG GTT AAC GGA TGC ACC AGC AAG AAA CTA GAG GGT GCA GAA ATA	619
Gly Met Val Asn Gly Cys Thr Ser Lys Lys Leu Glu Gly Ala Glu Ile	
40 45 50	

0975456 040600



**Table 1.** Mean values of the variables measured during the three trials

(xi) DESCRIPTION OF THE SEQUENCES: SEQ ID No: 3:

ATG	AAA	GGT	ATT	TCT	AAG	GTT	CTC	TCA	GCC	TCT	ATT	GTC	CTA	ATG	AAG	48
Met	Lys	Gly	Ile	Ser	Lys	Val	Leu	Ser	Ala	Ser	Ile	Val	Leu	Met	Lys	
1				5					10					15		
TTG	AAG	GGT	GTC	TAT	TCT	ACA	ACT	GTG	CTG	TGT	GGA	GAT	TCA	ACA	CAA	96
Leu	Lys	Gly	Val	Tyr	Ser	Thr	Thr	Val	Leu	Cys	Gly	Asp	Ser	Thr	Gln	
			20					25					30			
GGA	CTG	CAG	GGC	ACA	ACC	CAA	CCG	TCA	TAT	GTG	CTG	GTT	CCT	AGT	GCA	144
Gly	Leu	Gln	Gly	Thr	Thr	Gln	Pro	Ser	Tyr	Val	Leu	Val	Pro	Ser	Ala	
		35					40					45				
CCA	GAG	ACA	ATA	GCC	AAC	TGT	GGA	TAC	AGT	CCA	CAG	AAC	ATG	TAT	GTC	192
Pro	Glu	Thr	Ile	Ala	Asn	Cys	Gly	Tyr	Ser	Pro	Gln	Asn	Met	Tyr	Val	
	50					55					60					
CCT	TCT	ACT	CCT	ACT	ACC	ATG	CCT	TCC	ACA	GTG	CCA	GGC	ACA	ACT	GGT	240
Pro	Ser	Thr	Pro	Thr	Thr	Met	Pro	Ser	Thr	Val	Pro	Gly	Thr	Thr	Gly	
65					70					75					80	
GAG	AGC	GAG	ACA	CCT	ACT	TCT	CCA	ACA	TCA	TCT	CCT	ACA	GAG	GAT	GTG	288
Glu	Ser	Glu	Thr	Pro	Thr	Ser	Pro	Thr	Ser	Ser	Pro	Thr	Glu	Asp	Val	
				85					90					95		
GGA	ACA	TGC	AAG	ATT	GCT	GTT	GTA	AAG	CAT	TGT	GAT	GCA	CCA	GGA	ACA	336
Gly	Thr	Cys	Lys	Ile	Ala	Val	Val	Lys	His	Cys	Asp	Ala	Pro	Gly	Thr	
			100					105					110			
TCA	TCA	ACA	CCT	TGC	GAA	CCG	GAA	CAG	ACT	TTG	GCC	CCC	TCT	CAG	CCA	384
Ser	Ser	Thr	Pro	Cys	Glu	Pro	Glu	Gln	Thr	Leu	Ala	Pro	Ser	Gln	Pro	
			115					120					125			
GTA	GCA	GCT	ACA	ATT	GCC	ACA	CCA	CTG	GTT	GTT	GCT	TCT	GTG	CAG	ACG	432
Val	Ala	Ala	Thr	Ile	Ala	Thr	Pro	Leu	Val	Val	Ala	Ser	Val	Gln	Thr	
			130				135						140			
CCG	CAA	GCA	GCT	GTT	ACC	ATC	CTT	ACT	CCA	AAG	GCC	GTC	TCT	GCC	CAG	480
Pro	Gln	Ala	Ala	Val	Thr	Ile	Leu	Thr	Pro	Lys	Ala	Val	Ser	Ala	Gln	
145					150					155					160	

CCG GCA ACC ATC ATT TCA TTC AAC CAG GCA CCA GGC TAC AAT	528
Pro Ala Thr Ile Ile Ser Pro Phe Asn Gln Ala Pro Gly Tyr Tyr Asn	
165 170 175	
AGT GCA ATT CCC GGG CAA ATA CTT ACA GGT AAT GTT CTC TCT CCA AGT	576
Ser Ala Ile Pro Gly Gln Ile Leu Thr Gly Asn Val Leu Ser Pro Ser	
180 185 190	
GCC TCT TCT TGC CAA GTG GTG CCC GGA ACA ACA GGA AGC TCC ACC CCC	624
Ala Ser Ser Cys Gln Val Val Pro Gly Thr Thr Gly Ser Ser Thr Pro	
195 200 205	
CAG CAG CTA CCA GGC GCT GTT TCA TCT GGA ACC ATT CCT TGC CAA ATA	672
Gln Gln Leu Pro Gly Ala Val Ser Ser Gly Thr Ile Pro Cys Gln Ile	
210 215 220	
GTA CAG GGA ACT CAA AGT AGC GGA AAC ACC CCT GGA CAG CAA TTC TTG	720
Val Gln Gly Thr Gln Ser Ser Gly Asn Thr Pro Gly Gln Gln Phe Leu	
225 230 235 240	
CCG GGA ATC GTT CCT GTT GGA AGC CTC CAG CCG GAT CAA GCT ACT TCT	768
Pro Gly Ile Val Pro Val Gly Ser Leu Gln Pro Asp Gln Ala Thr Ser	
245 250 255	
GGA ACC CCT ACC CCT TCT GTT AGC CAA AGC CAA TCT GGA CAG CAA TGC	816
Gly Thr Pro Thr Pro Ser Val Ser Gln Ser Gln Ser Gly Gln Gln Cys	
260 265 270	
TGC TGC ACT CCT CCA ATC ACA AAC CCT GTA ATG CCA ACT CCT ATG GGT	864
Cys Cys Thr Pro Pro Ile Thr Asn Pro Val Met Pro Thr Pro Met Gly	
275 280 285	
ATC AGC AGT AAT GGG TAT CCC AGC TCA ACT GCG TAC GCC CCA ACC CTT	912
Ile Ser Ser Asn Gly Tyr Pro Ser Ser Thr Ala Tyr Ala Pro Thr Leu	
290 295 300	
GGA CAA TTG GGA CCT TGC ATC GAC ACA CAG AAG TCA ACA TCA TCC TGC	960
Gly Gln Leu Gly Pro Cys Ile Asp Thr Gln Lys Ser Thr Ser Ser Cys	
305 310 315 320	
GAA CCA AAA GAA AAG CCT GTA GCA CAG TAT GGA ATG GAA GCA TGC GCT	1008
Glu Pro Lys Glu Lys Pro Val Ala Gln Tyr Gly Met Glu Ala Cys Ala	
325 330 335	
GCA CCA ACT CCA ACT GCT GTT CTA GGA AAT GCT GAG TAT CTC CTT AGC	1056
Ala Pro Thr Pro Thr Ala Val Leu Gly Asn Ala Glu Tyr Leu Leu Ser	
340 345 350	
CCG GGG ATG TAT AAT TCA CTC AAC TCT CCA TGC AAC GCT TGC TGC CAA	1104
Pro Gly Met Tyr Asn Ser Leu Asn Ser Pro Cys Asn Ala Cys Cys Gln	
355 360 365	
CAA CAA TGC TAG	1116
Gln Gln Cys *	
370 371	

(2) INFORMATION FOR SEQ ID No: 4

(i) CHARACTERISTICS OF THE SEQUENCE:

(A) LENGTH:

(B) TYPE: nucleotide

(C) NUMBER OF STRANDS: double

(D) CONFIGURATION: linear  
(ii) TYPE OF MOLECULE: DNA  
(ix) CHARACTERISTICS  
(A) NAME/KEY:  
(xi) DESCRIPTION OF THE SEQUENCES: SEQ ID No: 4:

ATG TTG TTA CTT CTC TCA GCA GTT GCT TTT GTT AGC GCT ACA GCA GTC	48
Met Leu Leu Leu Leu Ser Ala Val Ala Phe Val Ser Ala Thr Ala Val	
1 5 10 15	
CAG TCA GGT GTT GTC TCC CAG CCT ACA ACA CCC ATT CCG ATT CTT CCT	96
Gln Ser Gly Val Val Ser Gln Pro Thr Thr Pro Ile Pro Ile Leu Pro	
20 25 30	
GGA CAG CCG ATG GGG GGC ATG GCC AAC GGG TGC ACT AAC AAG AAA CTA	144
Gly Gln Pro Met Gly Gly Met Ala Asn Gly Cys Thr Asn Lys Lys Leu	
35 40 45	
GAT GGT GTT GAA ATA ATG AGA AGG AAC ATG GTG GAA TGC CAG AAG AGA	192
Asp Gly Val Glu Ile Met Arg Arg Asn Met Val Glu Cys Gln Lys Arg	
50 55 60	
AAT GCA GAG GCA ACA AAA GCA ATG GTT GAA AGG GCT AAT GAA AAG GCT	240
Asn Ala Glu Ala Thr Lys Ala Met Val Glu Arg Ala Asn Glu Lys Ala	
65 70 75 80	
GTA GAA ACA TTC AAT AAG GAG GTC AGT AAA GGA CCT CAA AAG GAA AGC	288
Val Glu Thr Phe Asn Lys Glu Val Ser Lys Gly Pro Gln Lys Glu Ser	
85 90 95	
GGC CAG TGC ATA GAA AAA GCT GTA CAG GGC ACC GAC AGA TGT ATT CTT	336
Gly Gln Cys Ile Glu Lys Ala Val Gln Gly Thr Asp Arg Cys Ile Leu	
100 105 110	
GCA GGA ATA ATT GAT AAG GCT GTG AAC AAG CGT AAG TAC AGA ATC TCG	384
Ala Gly Ile Ile Asp Lys Ala Val Asn Lys Arg Lys Tyr Arg Ile Ser	
115 120 125	
GAT GTG GAG AAT AGC ACC TCG CTC TAT AGA GGC GAC AAA CTA ATT GCT	432
Asp Val Glu Asn Ser Thr Ser Leu Tyr Arg Gly Asp Lys Leu Ile Ala	
130 135 140	
CTA ATT GTC AAT GTT GAC TAT GGA CTT CAG CCA ATT ATC AAA CCA AAG	480
Leu Ile Val Asn Val Asp Tyr Gly Leu Gln Pro Ile Ile Lys Pro Lys	
145 150 155 160	
AAG AAG AAA TCC AAG ATA ATG GCA AAT CTT CCT CAA CCA AAG AGA GAG	528
Lys Lys Lys Ser Lys Ile Met Ala Asn Leu Pro Gln Pro Lys Arg Glu	
165 170 175	
ATG TAT TTC AAC CAG ATC GGA CAG CTT GTT GGA GCA AAG GGA ACA TTC	576
Met Tyr Phe Asn Gln Ile Gly Gln Leu Val Gly Ala Lys Gly Thr Phe	
180 185 190	
CCT CAA GAC AAC AAG GAT GAA TGC AAG CCA TGC GAA CCT AAG AAG ACT	624
Pro Gln Asp Asn Lys Asp Glu Cys Lys Pro Cys Glu Pro Lys Lys Thr	
195 200 205	
GTT GAA ACT GCT TCT GAA AGA TGT AAT CTT GGG TGC GAG CTT AAG GGA	672
Val Glu Thr Ala Ser Glu Arg Cys Asn Leu Gly Cys Glu Leu Lys Gly	
210 215 220	





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